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Key indicators

Single-crystal X-ray study
 $T = 180$ K
Mean $\sigma(\text{C}-\text{C}) = 0.006$ Å
 R factor = 0.062
 wR factor = 0.168
Data-to-parameter ratio = 10.3

For details of how these key indicators were automatically derived from the article, see <http://journals.iucr.org/e>.

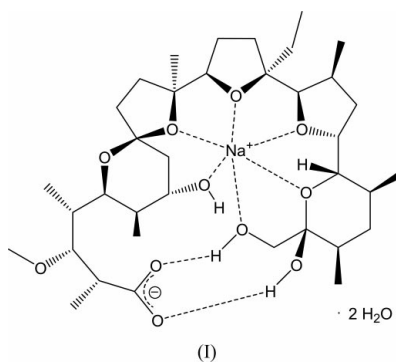
Sodium monensin dihydrate

The crystal structure of the title compound, $[\text{Na}(\text{C}_{36}\text{H}_{61}\text{O}_{11})] \cdot 2\text{H}_2\text{O}$, was first reported by Duax *et al.* [*J. Am. Chem. Soc.* (1980), **102**, 6725–6729]. We report here the crystal structure of a new polymorph, determined at the low temperature of 180 (2) K, in the same orthorhombic non-centrosymmetric space group $P2_12_12_1$. The structure contains one crystallographically unique sodium monensin complex, showing a highly distorted octahedral coordination environment for Na^+ , forming undulating layers in the ac plane. H atoms from the pendant hydroxyl groups involved in head-to-tail hydrogen bonding with the carboxylate group and from the crystallization water molecules occupying the interlayer spaces have been successfully located in difference Fourier maps.

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Comment

Monensin is a commercially important polyether ionophoric antibiotic, first isolated by Agtarap *et al.* (1967). Ionophoric antibiotics readily complex alkali and alkaline earth metal ions *via* their tetrahydrofuran O atoms to create shell-like complexes. These complexes act *in vivo* as membrane transporters to create a pH gradient that leads to cell death. In addition to antibiotic activity, monensin is also widely used in livestock as a growth promoter and specifically as a coccidiostat in poultry. A search in the Cambridge Structural Database (Version 5.24; Allen, 2002), reveals that the first crystal structures of sodium monensin complexes (an anhydrous form and a dihydrate) were reported by Duax *et al.* (1980). Further structural studies on monensin determined the stereochemistry of the 18 chiral centres (Robinson & Ajaz, 1987) and the NMR solution state conformation (Martinek *et al.*, 2000).



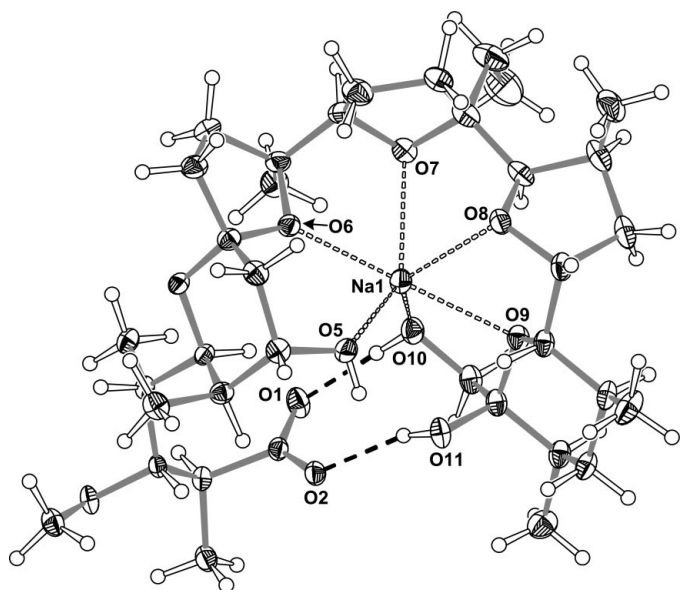


Figure 1
Perspective view of the sodium monensin complex, with all non-H atoms represented as displacement ellipsoids drawn at the 30% probability level, and H atoms shown as small spheres with arbitrary radius. The two crystallization water molecules have been omitted for clarity. Head-to-tail hydrogen bonds between the pendant hydroxyl groups and the carboxylate group are represented as black-filled dashed bonds (for hydrogen-bonding details, see Table 2).

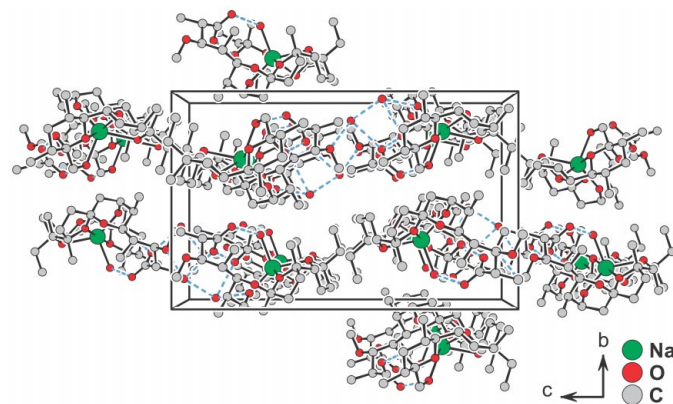


Figure 2
Perspective view along the *a* axis of (I). The sodium monensin complexes form undulating layers in the *ac* plane which alternate in the *b* axis direction in an *ABAB*... fashion, and are intercalated by the crystallization water molecules which establish hydrogen-bonding bridges between neighbouring complexes within the same layer. Hydrogen bonds are represented as blue-filled dashed lines (for hydrogen-bonding details, see Table 2). H atoms have been omitted for clarity.

facile comparison and elucidation of the stereochemistry of the chiral centres, and the participation of the pendant hydroxyl groups in metal coordination. As part of our research, we came upon a different polymorph for sodium monensin dihydrate, (I), which we report here.

Just like the first sodium monensin dihydrate structure reported by Duax *et al.* (1980), (I) also crystallizes in the non-centrosymmetric orthorhombic space group $P2_12_12_1$, with one whole complex and two water molecules in the asymmetric unit (Fig. 1). Also here, the Na^+ centre is coordinated to six O atoms in a geometry which is best described as a highly distorted octahedron (Fig. 1 and Table 1). The Na—O bonds, ranging between 2.336 (4) and 2.520 (3) Å (Table 1), are in very good agreement with the values found by Duax and co-workers [2.336 (7)–2.543 (7) Å]. Intramolecular head-to-tail hydrogen bonding between the pendant hydroxyl groups and the carboxylate group [O10...O1 = 2.643 (4) Å and O11...O2 = 2.665 (4) Å], leads to the formation of a shell-like complex which completely traps the metal centre within the monensin ligand (Fig. 1). Exactly the same was observed in the determination of the earlier polymorph, with calculated *D*...*A* distances of 2.51 and 2.64 Å (Duax *et al.*, 1980). Individual sodium complexes close pack in the *ac* plane, leading to the formation of undulated layers which alternate in an *ABAB*... fashion in the *b* axis direction (two layers per axis repeat) (Fig. 2). The crystallization water molecules occupy interlayer spaces and are involved in O—H...O and O—H...O[−] interactions which link together neighbouring sodium complexes within the same layer (Fig. 2 and Table 2).

Experimental

Monensin sodium salt was purchased from Aldrich (95% purity) and used without further purification. Crystals suitable for X-ray diffraction analysis were obtained by recrystallization from distilled water.

Crystal data

[Na(C₃₆H₆₁O₁₁)]·2H₂O
M_r = 728.87
 Orthorhombic, $P2_12_12_1$
a = 12.4768 (4) Å
b = 14.1024 (4) Å
c = 22.1653 (7) Å
V = 3900.0 (2) Å³
Z = 4
D_x = 1.241 Mg m^{−3}

Mo *K*α radiation
 Cell parameters from 73775 reflections
 θ = 1.0–27.5°
 μ = 0.10 mm^{−1}
T = 180 (2) K
 Block, colourless
 0.46 × 0.12 × 0.07 mm

Data collection

Nonius KappaCCD diffractometer
 Thin-slice ω and φ scans
 Absorption correction: multi-scan (SORTAV; Blessing, 1995)
 $T_{\text{min}} = 0.937$, $T_{\text{max}} = 0.984$
 14637 measured reflections
 4873 independent reflections

4132 reflections with $I > 2\sigma(I)$
 $R_{\text{int}} = 0.048$
 $\theta_{\text{max}} = 27.5^\circ$
 $h = -16 \rightarrow 16$
 $k = -12 \rightarrow 18$
 $l = -28 \rightarrow 28$

Refinement

Refinement on F^2
 $R[F^2 > 2\sigma(F^2)] = 0.062$
 $wR(F^2) = 0.168$
 $S = 1.12$
 4873 reflections
 472 parameters
 H atoms treated by a mixture of independent and constrained refinement

$w = 1/[\sigma^2(F_o^2) + (0.0807P)^2 + 2.259P]$
 where $P = (F_o^2 + 2F_c^2)/3$
 $(\Delta/\sigma)_{\text{max}} < 0.001$
 $\Delta\rho_{\text{max}} = 0.69 \text{ e \AA}^{-3}$
 $\Delta\rho_{\text{min}} = -0.56 \text{ e \AA}^{-3}$

Table 1
Selected geometric parameters (Å, °).

Na1—O5	2.336 (4)	Na1—O8	2.463 (3)
Na1—O6	2.365 (3)	Na1—O7	2.520 (3)
Na1—O10	2.373 (3)	O1—C1	1.242 (5)
Na1—O9	2.459 (3)	O2—C1	1.263 (5)
O5—Na1—O6	75.79 (11)	O10—Na1—O8	122.75 (12)
O5—Na1—O10	117.65 (13)	O9—Na1—O8	64.82 (10)
O6—Na1—O10	112.69 (12)	O5—Na1—O7	136.28 (13)
O5—Na1—O9	103.59 (12)	O6—Na1—O7	68.42 (10)
O6—Na1—O9	178.44 (12)	O10—Na1—O7	99.19 (12)
O10—Na1—O9	68.87 (10)	O9—Na1—O7	111.51 (12)
O5—Na1—O8	104.57 (12)	O8—Na1—O7	69.84 (10)
O6—Na1—O8	113.87 (11)		

Table 2
Hydrogen-bonding geometry (Å, °).

<i>D</i> —H... <i>A</i>	<i>D</i> —H	H... <i>A</i>	<i>D</i> ... <i>A</i>	<i>D</i> —H... <i>A</i>
O5—H5...O13	0.84 (2)	2.04 (3)	2.810 (7)	152 (5)
O10—H10...O1	0.84 (2)	1.81 (2)	2.643 (4)	170 (8)
O11—H11...O2	0.84	1.88	2.665 (4)	156
O12—H12E...O2	0.90 (2)	1.90 (2)	2.791 (4)	174 (5)
O12—H12D...O3 ⁱ	0.91 (2)	2.05 (3)	2.907 (4)	157 (5)
O13—H13B...O11	0.986 (10)	2.04 (5)	2.882 (10)	142 (6)
O13—H13A...O12	0.988 (10)	1.96 (4)	2.769 (8)	137 (5)

Symmetry code: (i) $\frac{1}{2} + x, \frac{3}{2} - y, 1 - z$.

All H atoms bonded to carbon were placed in calculated positions (C—H = 0.98–1.00 Å) and allowed to ride during subsequent refinement with $U_{\text{iso}}(\text{H}) = xU_{\text{eq}}(\text{C})$ (with $x = 1.2$ for —CH and —CH₂—, and $x = 1.5$ for methyl groups). H atoms of the hydroxyl groups and of the crystallization water molecules were successfully located in difference Fourier maps. O—H and H...H distances were

restrained in order to ensure a chemically reasonable geometry for the hydroxyl groups and also to the water molecules. A total of 3597 estimated Friedel pairs were merged before refinement and not used as independent data. The Flack (1983) parameter was found to be meaningless and was omitted.

Data collection: *COLLECT* (Nonius, 1998); cell refinement: *HKL SCALEPACK* (Otwinowski & Minor, 1997); data reduction: *HKL DENZO* (Otwinowski & Minor, 1997) and *SCALEPACK*; program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); program(s) used to refine structure: *SHELXTL* (Bruker, 2001); molecular graphics: *SHELXTL*; software used to prepare material for publication: *SHELXTL*.

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